

AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions of claims in the application.

Listing of Claims:

1-29 (Canceled)

30. (Currently Amended) A method of lowering cholesterol in a mammal expressing a functional low density lipoprotein (LDL) receptor without inducing hypertriglyceridemia, said method comprising intravascularly administering to said mammal a replication-defective adenoviral ~~an expression vector~~ comprising a nucleic acid encoding a secreted polypeptide ~~comprising a region of at least 150 amino acids~~ having at least 90% sequence identity to ~~the corresponding region of amino acid residues 1-185 of SEQ ID NO:2~~, wherein said nucleic acid does not encode amino acids 260-299 of SEQ ID NO:2 and said polypeptide, when expressed in said mammal, lowers the total serum cholesterol level without inducing hypertriglyceridemia.

31-32 (Canceled)

33. (Currently Amended) The method of claim 30, wherein said nucleic acid is contained in a recombinant adenoviral ~~viral~~ vector.

34. (Original) The method of claim 33, wherein said vector is administered intravenously.

35. (Canceled)

36. (Original) The method of claim 33, wherein said vector is administered to an artery at the site of a lesion.

37-42 (Canceled)

43. (Original) The method of claim 30, wherein said mammal lacks an endogenous, normally functioning apoE gene.

44. (Original) The method of claim 30, wherein said mammal is at risk for developing atherosclerosis due to accumulation of lipoprotein remnants in the bloodstream.

45-46 (Canceled)

47. (Original) The method claim of 30, wherein said nucleic acid is administered to or expressed in the liver of said mammal.

48-50 (Canceled)

51. (Currently Amended) The method of claim 30, wherein said polypeptide region has 100% sequence identity to ~~the corresponding region of amino acid residues 1-185 of SEQ ID~~ NO:2.

52. (Canceled)

53. (Previously Presented) The method of claim 30, wherein said polypeptide further comprises a signal peptide.

54. (Currently Amended) The method of claim 30, wherein said polypeptide consists of between 185 ~~150~~ and 215 amino acids.

55. (Previously Presented) The method of claim 30, wherein said polypeptide consists of 203 amino acids.

56. (Previously Presented) The method of claim 30, wherein said nucleic acid encodes residues 1-203 of an apoE preprotein of any one of SEQ ID Nos. 14-19.

57. (Previously Presented) The method of claim 30, wherein said polypeptide consists of 220 amino acids.

58. (Previously Presented) The method of claim 30, wherein said nucleic acid encodes residues 1-220 of an apoE preprotein of any one of SEQ ID Nos. 14-19.

59. (Previously Presented) The method of claim 30, wherein said polypeptide consists of 247 amino acids.

60. (Previously Presented) The method of claim 30, wherein said nucleic acid encodes residues 1-247 of an apoE preprotein of any one of SEQ ID Nos. 14-19.

61. (Previously Presented) The method of claim 30, wherein said polypeptide consists of 277 amino acids.

62. (Previously Presented) The method of claim 30, wherein said nucleic acid encodes residues 1-277 of an apoE preprotein of any one of SEQ ID Nos. 14-19.

63. (Canceled)

64. (Previously Presented) The method of claim 30, wherein said region is identical to amino acid residues 1-185 of SEQ ID NO:2.

65. (Previously Presented) The method of claim 30, wherein said region has at least 90% sequence identity to amino acid residues 1-202 of SEQ ID NO:2.

66. (Previously Presented) The method of claim 65, wherein said region is identical to amino acid residues 1-202 of SEQ ID NO:2.

67. (Previously Presented) The method of claim 30, wherein said polypeptide is apoE3-202.

68. (Previously Presented) The method of claim 30, wherein said region has at least 90% sequence identity to amino acid residues 1-229 of SEQ ID NO:2.

69. (Previously Presented) The method of claim 65, wherein said region is identical to amino acid residues 1-229 of SEQ ID NO:2.

70. (Previously Presented) The method of claim 30, wherein said region has at least 90% sequence identity to amino acid residues 1-259 of SEQ ID NO:2.

71. (Previously Presented) The method of claim 70, wherein said region is identical to amino acid residues 1-259 of SEQ ID NO:2.

72. (Previously Presented) The method of claim 53, wherein said signal peptide comprises a polypeptide having the amino acid sequence of SEQ ID NO: 13.

73-78 (Cancelled)